

Figure 1: 108P5H8 SSH sequence of 448 nucleotides (SEQ ID: 2568)

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1  GATCCAGATT TCTCTGCACA CTGGACTTCG TAGAGTAAGT GTGGTAGACA AAGAGACTAC
61  ACTGCACAAC CACCAAGTGAA TATCATTGCT AAGAAGACTT TGGGTCGTGT TTCTCAGCCA
121 CTCTCAGCAGC TTTTGTAGAC TTATTTGATT TTGAAACAAG CAGTTAGCTA AATCTATTTT
181 CCTTTTATGC ATATATGTTA ATTGGCTCAA CTTAATATGG TGTCTTTACA GAATATGAGC
241 CCATTTGAAA TAAGGTTTTA GGCAATTGTC CTGTGGCTC TGATTGTAT ATAGCAAATT
301 TAAAGGTACA GAGTGTTCCT TAGATAGAAG ATTAGTCAT TTGGTTCCAT TTGCTTTTGA
361 AGCAAGCCAA GCTCATGAGC CAGTTGGTTA TTTGTCATA ATGAACACCC ATCACTATAT
421 GCTATGTTGA GGGGAGGCAA GGCTGATC

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Figure 2A. The cDNA (SEQ ID. NO. :2569) and amino acid sequence (SEQ ID. NO. :2570) of 108P5H8 v.1. The start methionine is underlined. The open reading frame extends from nucleic acid 253-1542 including the stop codon.

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1  ggcggcctccagcagcgggcgcgcgggcgcgagcagacccacctctcctgcggcgcg
61  ggtggagcagcgcgagcccgctcgctgagccggccggggcggggagatgagttgcggc
121  cccggcgagcgccccaggatggggagggaacgcgcggcactgcccctcgagaactggcgct
181  ccggtgaagtggcgccgcggcggtccgctcccccaagcggttcgcacccgcggcgcg
1      M A G S G A W K R L K S M L R K
241  tcagcctctgccATGGCCGGCTCTGGCGCTGGAAGCGCCTCAAATCTATGCTAAGGAAG
17  D D A P L F L N D T S A F D F S D E A G
301  GATGATGCGCCGCTGTTTTAAATGACACCGCGCCTTTGACTTCTCGGATGAGCGGGG
37  D E G L S R F N K L R V V A D D G S E
361  GACGAGGGGCTTCTCGGTTCAACAACACTTCGAGTTTGGTGGCCGATGACGGTCCGAA
57  A P E R P V N G A H P T L Q A D D D S L
421  GCCCCGAAAGCCCTGTTAACGGGGCGACCCGACCTCCAGGCCGACGATGATTCTTA
77  L D Q D L P L T N S Q L S L K V D S C D
481  CTGGACCAAGACTTACCTTTGACCAACAGTCAGCTGAGTTTGAAGGTGGAATCCTGTGAC
97  N C S K Q R E I L K Q R K V K A R L T I
541  AACTGCGACCAACAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATT
117  A A V L Y L L F M I G E L V G G Y I A N
601  GCTGCCGTCTGCTACTTGCTTTTCATGATTGGAGAATTTGAGGTGGATACATTGCAAAT
137  S L A I M T D A L H M L T D L S A I I L
661  AGCCTAGCAATCATGACAGATGCACCTTCATATGTTAACTGACCTAAGCGCCATCACTC
157  T L L A L W L S S K S P T K R F T F G F
721  ACCCTGCTTGCTTTGTGGCTATCATCAAAATCACCAACCAAAAGATTACCTTTGGATT
177  H R L E V L S A M I S V L L V Y I L M G
781  CATCGCTTAGAGGTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTATTGGGA

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197 F L L Y E A V Q R T I H M N Y E I N G D
 841 TTCCTCTTATATGAAGCTGTGCAAAGAAGTATCCATATGAAGTATGAAATAAATGGAGAT
 217 I M L I T A A V G V A V N V I M G F L L
 901 ATAATGCTCATACCGCAGCTGTGGAGTTGAGTTAATGTAATAATGGGGTTTCTGTG
 237 N Q S G H R H S H S H S L P S N S P T R
 961 AACCAGTCTGGTCCCGTCACTCCCATTCCTCCCTGCCTTCAAAATCCCTACCAGA
 257 G S G C E R N H G Q D S L A V R A A F V
 1021 GGTTCGGGTGTGAACGTAAACATGGGCAGGATAGCTGGCAGTGAGAGCTGCAATTGTA
 277 H A L G D L V Q S V G V L I A A Y I I R
 1081 CATGCTTTGGGAGATTTGGTACAGAGTGTGGTGCTAATAGCTGCATACATCATACGA
 297 F K P E Y K I A D P I C T Y V F S L L V
 1141 TTCAAGCCGAATAACAAGATTGCTGACCCCATCTGTACATACGTATTTTCATTACTTGTG
 317 A F T T F R I I W D T V V I I L E G V P
 1201 GCTTTTACAACATTTGAAATCATATGGGATACAGTAGTTATAATACTAGAAAGCTGTGCCA
 337 S H L N V D Y I K E A L M K I E D V Y S
 1261 AGCCATTTGAATGTAGACTATATCAAGAAGCCTTGATGAAATAGAAGATGTATATTC
 357 V E D L N I W S L T S G K S T A I V H I
 1321 GTCGAAGATTTAAATATCTGGTCTCTCACTTCAGGAAAACTACTGCCATAGTTCACATA
 377 Q L I P G S S S K W E E V Q S K A N H L
 1381 CAGCTAATCTCGAAGTTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAAACATTTA
 397 L L N T F G M Y R C T I Q L Q S Y R Q E
 1441 TTATTGAACACATTTGGCATGTATAGATGTACTATTACAGCTTACAGAGTTACAGGCAAGAA
 417 V D R T C A N C Q S S S P *
 1501 GTGGACAGAACTTGTGCAAATTTGTCAGAGTTCTAGTCCCTAATTTtgatattttgggaa
 1561 ctccctgcttatttctcctgcagtcacagacttgagagcaataaatgcaaaccttaaatga
 1621 gaaaatggaaatccctgacagctgtgtccgtatcaagcatcagctctcctcaaacagttgccc
 1681 cagcctgacagtgctagtctctgtttaaaggtaaaggagactttgccataatttcaga
 1741 tgaagatgtttcccaaacactgtttacagaatgagatgtgactctacagatacctcatag
 1801 aagacaatccaagatcatacttcattaaacttgacagagtagctgtcttaaggaaagcatc
 1861 aagaattcaatatttgcatattaaaaatacttttaaggccattttatattaaagccagtgc
 1921 tggaaaaactgaattttttattattgtataataatctcgacacccagctctctggaattgc
 1981 tgcttctcttttacagaaattactaccacaagatttcaggaaagtactagtagttatccc
 2041 aaaagtggaataagcatgtattcctaagtggttcagaaaatgttttatttcacacataagt
 2101 cttaatgttattgttatgattatactttataaaacaaccttttccagatgctcaggggtt
 2161 tgaatctcaagttaacatttttctatttattgtaatcttagaaccaatctttattatt
 2221 gtggtcactgttattaaatgatttaggaaatactttcaatattattctgaatggctgaag
 2281 ttagtcttaaaactcaaatattactatgatgatttataaaacaaaataaaagagcgaggtgg
 2341 qgaaaaaaaaaaaaaaaaaaaaa

Figure 2B. The cDNA (SEQ ID. NO. :2571) and amino acid sequence (SEQ ID. NO. :2572) of 108P5H8 v.2. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

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1 M A G S G A W K R L K S M L R K D D A P
1 ATGCCGGCTCTGGCGCTGGAAGCGCCTCAAATCTATGCTAAGGAAGGATGATGCGCGG
21 L F L N D T S A F D F S D E A G D E G L
61 CTGTTTTTAATGACACCGCGCTTTGACTTCTCGGATGAGCGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAACTTCGAGTTGTGTGGCCGATGACGGTTCGAAGCCCGGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAAGGGGCGCACCCGACCTCCAGGCCGACGATGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTACCCCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATCAAAATCACCMCCAAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTGAGCTATGATTAGTGTGCTTGTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAGAAGCTATCCATATGAAGCTATGAAATAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGAGCTGTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACAGCTTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATCCCACTCCCTGCCTTCAAATTCCTACAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAAACATGGGCAGGATAGCCTGGCAGTGAGAGCTGCATTGTACATGCTTTGGGA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATTTGGTACAGAGTGTGGTGTGCTAATAGCTGCATACATACGATTCAAGCCAGAA
301 Y K I A D P I C T Y V F S L L V A F T T
901 TACAAGATTGCTGATCCCATCTGTACATACGTATTTTCATTACTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
961 TTTGCAATCATATGGGATACAGTAGTTATAATACTAGAAGGTGTGCCAAGCCATTTGAAT
341 V D Y I K E A L M K I E D V Y S V E D L

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1021 GTAGACTATATCAAAGAAGCCTTGATGAAAATAGAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTACAGTTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATTGTCAGAGTTCTAGTCCCTAAttttatgtattttggggactcctgccttat
1321 ttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaaaatggaatc
1381 cctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagcctgacagt
1441 gctagtcctctgtttaatggtaaaaggagactttgccataattttcagatgaagatgtttc
1501 ccaaacactgtttacagaatgagatgtgactctacagatacctcatag

Figure 2C. The cDNA (SEQ ID. NO. :2573) and amino acid sequence (SEQ ID. NO. :2574) of 108P5H8 v.3. The start methionine is underlined. The open reading frame extends from nucleic acid 1-1290 including the stop codon.

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1  M A G S G A W K R L K S M L R K D D A P
1  ATGGCCGGCTCTGGCGCGTGGGAAGCGCTCAAATCTATGCTAAGGAAGGATGATGCGCCG
21 L F L N D T S A F E F S D E A G D E G L
61 CTGTTTTTAAATGACACGCGCCTTGAGTTCCTCGATGAGCGGGGGACGAGGGGCTT
41 S R F N K L R V V V A D D G S E A P E R
121 TCTCGGTTCAACAAACTTCGAGTTGTGGTGGCCGATGACGGTTCCGAAGCCCCGAAAGG
61 P V N G A H P T L Q A D D D S L L D Q D
181 CCTGTTAAGCGGGCGCACCAGCCCTCCAGGCCGACGATTCCTTACTGGACCAAGAC
81 L P L T N S Q L S L K V D S C D N C S K
241 TTACCTTTGACCAACAGTCAGCTGAGTTTGAAGTGGACTCCTGTGACAACTGCAGCAAA
101 Q R E I L K Q R K V K A R L T I A A V L
301 CAGAGAGAGATACTGAAGCAGAGAAAGGTGAAAGCCAGGTTGACCATTGCTGCCGTTCTG
121 Y L L F M I G E L V G G Y I A N S L A I
361 TACTTGCTTTTCATGATTGGAGAACTTGTAGGTGGATACATTGCAAAATAGCCTAGCAATC
141 M T D A L H M L T D L S A I I L T L L A
421 ATGACAGATGCACTTCATATGTTAACTGACCTAAGCGCCATCATACTACCCCTGCTTGCT
161 L W L S S K S P T K R F T F G F H R L E
481 TTGTGGCTATCATAAAATCACCACCAAAAGATTACCTTTGGATTTCATCGCTTAGAG
181 V L S A M I S V L L V Y I L M G F L L Y
541 GTTTTGTCAGCTATGATTAGTGTGCTGTTGGTGTATATACTTATGGGATTCCTCTTATAT
201 E A V Q R T I H M N Y E I N G D I M L I
601 GAAGCTGTGCAAGAATACTATCCATATGAACATGAAATAAATGGAGATATAATGCTCATC
221 T A A V G V A V N V I M G F L L N Q S G
661 ACCGAGCTGTTGGAGTTGCAGTTAATGTAATAATGGGGTTTCTGTTGAACAGCTGGT
241 H R H S H S H S L P S N S P T R G S G C
721 CACCGTCACTCCCATCCCACTCCCTGCCTTCAAATCCCCCTACCAGAGGTTCTGGGTGT
261 E R N H G Q D S L A V R A A F V H A L G
781 GAACGTAACCTGGGCAGGATAGCCTGGCAGTGAGAGCTGCAATTTGACATGCTTTGGCA
281 D L V Q S V G V L I A A Y I I R F K P E
841 GATCTGGTACAGAGTGTTGGTGTGCTAATAGCTGCATACATACGATTACAAGCCAGAA
901 Y K A I A D P I C T Y V F S L L V A F T A
961 TTTCAAGATTGCTGACCCATCTGTACATACGATTTTTCATTACTTGTGGCTTTTACAACA
321 F R I I W D T V V I I L E G V P S H L N
961 TTTCAAGATCATATGGGATACAGTAGTTATAATACTAGAGGTGCGCAAGCCATTTGAAT
  
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341 V D Y I K E A L M K I E D V Y S V E D L
1021 GTAGACTATATCAAGAAGCCTTGATGAAAAAGATGTATATTCAGTCGAAGATTTA
361 N I W S L T S G K S T A I V H I Q L I P
1081 AATATCTGGTCTCTCACTTCAGGAAAATCTACTGCCATAGTTCACATACAGCTAATTCCT
381 G S S S K W E E V Q S K A N H L L L N T
1141 GGAAGTTCATCTAAATGGGAGGAAGTACAGTCCAAAGCAAACCATTTATTATTGAACACA
401 F G M Y R C T I Q L Q S Y R Q E V D R T
1201 TTTGGCATGTATAGATGTACTATTTCAGCTTCAGAGTTACAGGCAAGAAGTGGACAGAACT
421 C A N C Q S S S P *
1261 TGTGCAAATGTGTCAGAGTTCTAGTCCCTAATtttatgtattgttttagcattgctgaatt
1321 cactttatttatcctgcagtcacagacttgagagcaataaatgcaaacctaaatgagaaa
1381 atggaatccctgacagctgtgtccgtatcaagcatcagtcctctcaaacagttgccccagc
1441 ctgacagtgctagtcctctgtttaatggtaaaaggagactttgcccataattttcagatgaa
1501 gatgtttcccaaacactgtttacagaatgagatgtgactcctacagatcacctcatag

Figure 4:

Figure 4a. Nucleic acid sequence alignment of the 3 variants of 108P5H8. (SQ ID Nos: 2569, 2571 & 2573). Highlighted in yellow and underlined are the variations between the variants. The ORF extends from nucleotides 253-1542 of 108P5H8 v.1.

1	15 16	30 31	45 46	60 61	75 76
v. 1	GC	GC	GC	GC	GC
v. 2	GC	GC	GC	GC	GC
v. 3	GC	GC	GC	GC	GC
91	105 106	120 121	135 136	150 151	165 166
v. 1	CG	CG	CG	CG	CG
v. 2	CG	CG	CG	CG	CG
v. 3	CG	CG	CG	CG	CG
181	195 196	210 211	225 226	240 241	255 256
v. 1	CG	CG	CG	CG	CG
v. 2	CG	CG	CG	CG	CG
v. 3	CG	CG	CG	CG	CG
271	285 286	300 301	315 316	330 331	345 346
v. 1	TG	TG	TG	TG	TG
v. 2	TG	TG	TG	TG	TG
v. 3	TG	TG	TG	TG	TG
361	375 376	390 391	405 406	420 421	435 436
v. 1	GAC	GAC	GAC	GAC	GAC
v. 2	GAC	GAC	GAC	GAC	GAC
v. 3	GAC	GAC	GAC	GAC	GAC
451	465 466	480 481	495 496	510 511	525 526
v. 1	CG	CG	CG	CG	CG
v. 2	CG	CG	CG	CG	CG
v. 3	CG	CG	CG	CG	CG

**TITLE: NUCLEIC ACID AND ENCODED ZINC TRANSPORTER
PROTEIN ENTITLED 108P5H8 USEFUL IN TREATMENT
AND DETECTION OF CANCER**

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541	555 556	570 571	585 586	600 601	615 616	630
V.1	AACTGCAGCAACAG	AGAGATACCTGAG	CAGAGAAAGGTGAAA	GCCAGGTGTGACATT	GCTGCCGTTCTGTAC	TTCGTTTTCATGATT
V.2	AACCTGCAGCAACAG	AGAGATACCTGAG	CAGAGAAAGGTGAAA	GCCAGGTGTGACATT	GCTGCCGTTCTGTAC	TTCGTTTTCATGATT
V.3	AACCTGCAGCAACAG	AGAGATACCTGAG	CAGAGAAAGGTGAAA	GCCAGGTGTGACATT	GCTGCCGTTCTGTAC	TTCGTTTTCATGATT
631	645 646	660 661	675 676	690 691	705 706	720
V.1	GGAGACTGTGAGT	GGATACATTCGAAT	AGCCTAGCAATCATG	ACAGATGCACTTCAT	ATGTTAACTGACCTA	AGGCCATCATCTC
V.2	GGAGACTGTGAGT	GGATACATTCGAAT	AGCCTAGCAATCATG	ACAGATGCACTTCAT	ATGTTAACTGACCTA	AGGCCATCATCTC
V.3	GGAGACTGTGAGT	GGATACATTCGAAT	AGCCTAGCAATCATG	ACAGATGCACTTCAT	ATGTTAACTGACCTA	AGGCCATCATCTC
721	735 736	750 751	765 766	780 781	795 796	810
V.1	ACCGTCTGTGTTG	TGCTATCATCAAAA	TCACCAACCAAAAGA	TTACACCTTTTGANTT	CATCGCTTAGAGGT	TTCGTCAGCTAIGATT
V.2	ACCGTCTGTGTTG	TGCTATCATCAAAA	TCACCAACCAAAAGA	TTACACCTTTTGANTT	CATCGCTTAGAGGT	TTCGTCAGCTAIGATT
V.3	ACCGTCTGTGTTG	TGCTATCATCAAAA	TCACCAACCAAAAGA	TTACACCTTTTGANTT	CATCGCTTAGAGGT	TTCGTCAGCTAIGATT
811	825 826	840 841	855 856	870 871	885 886	900
V.1	AGTGTGCTGTGTTG	TATATACCTTATGGA	TTCTCTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACTAT	GAATATAATGAGAT
V.2	AGTGTGCTGTGTTG	TATATACCTTATGGA	TTCTCTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACTAT	GAATATAATGAGAT
V.3	AGTGTGCTGTGTTG	TATATACCTTATGGA	TTCTCTTATATGAA	GCTGTGCAAGAAGT	ATCCATATGAACTAT	GAATATAATGAGAT
901	915 916	930 931	945 946	960 961	975 976	990
V.1	ATAATGCTCATCACC	GCAGCTGTGAGGT	GCAGTTAATGTAA	ATGGGGTTTCTGTTG	AACCAGTCTGGTCC	GTCACCTCCCATCC
V.2	ATAATGCTCATCACC	GCAGCTGTGAGGT	GCAGTTAATGTAA	ATGGGGTTTCTGTTG	AACCAGTCTGGTCC	GTCACCTCCCATCC
V.3	ATAATGCTCATCACC	GCAGCTGTGAGGT	GCAGTTAATGTAA	ATGGGGTTTCTGTTG	AACCAGTCTGGTCC	GTCACCTCCCATCC
991	1005 1006	1020 1021	1035 1036	1050 1051	1065 1066	1080
V.1	CACCTCCCTGCCTTCA	AATCCCTCACCAGA	GGTTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCTGGCAGT	AGAGCTGCATTTTA
V.2	CACCTCCCTGCCTTCA	AATCCCTCACCAGA	GGTTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCTGGCAGT	AGAGCTGCATTTTA
V.3	CACCTCCCTGCCTTCA	AATCCCTCACCAGA	GGTTCTGGGTGTGAA	CGTAACCATGGGCAG	GATAGCTGGCAGT	AGAGCTGCATTTTA
1081	1095 1096	1110 1111	1125 1126	1140 1141	1155 1156	1170
V.1	CATCCTTTGGGAGAT	TTCGTACAGAGTGT	GGTGTCTAATAGCT	GCATACATCATACCA	TTCAGCCGCAATATC	AGAGTTGCTGTGCC
V.2	CATCCTTTGGGAGAT	TTCGTACAGAGTGT	GGTGTCTAATAGCT	GCATACATCATACCA	TTCAGCCGCAATATC	AGAGTTGCTGTGCC
V.3	CATCCTTTGGGAGAT	TTCGTACAGAGTGT	GGTGTCTAATAGCT	GCATACATCATACCA	TTCAGCCGCAATATC	AGAGTTGCTGTGCC
1171	1185 1186	1200 1201	1215 1216	1230 1231	1245 1246	1260

v.1	ATCTGTACATACGTA	TTTTCATTCTTG	GCTTTTACACATTT	CGAATCATATGGGAT	ACAGTAGTTATTA	CTAGAAGTGTGGCA
v.2	ATCTGTACATACGTA	TTTTCATTCTTG	GCTTTTACACATTT	CGAATCATATGGGAT	ACAGTAGTTATTA	CTAGAAGTGTGGCA
v.3	ATCTGTACATACGTA	TTTTCATTCTTG	GCTTTTACACATTT	CGAATCATATGGGAT	ACAGTAGTTATTA	CTAGAAGTGTGGCA
1261	1275 1276	1290 1291	1305 1306	1320 1321	1335 1336	1350
v.1	AGCCATTGCAATGTA	GACTAATCAAGAA	GCCTTGATGAAATA	GAAGATCTATATCA	GTCGAAGATTAAAT	ATCTGCTCTCTAC
v.2	AGCCATTGCAATGTA	GACTAATCAAGAA	GCCTTGATGAAATA	GAAGATCTATATCA	GTCGAAGATTAAAT	ATCTGCTCTCTAC
v.3	AGCCATTGCAATGTA	GACTAATCAAGAA	GCCTTGATGAAATA	GAAGATCTATATCA	GTCGAAGATTAAAT	ATCTGCTCTCTAC
1351	1365 1366	1380 1381	1395 1396	1410 1411	1425 1426	1440
v.1	TCAGGAAATCTACT	GCCATGTTTCACATA	CAGCTAATTCCTGGA	AGTTTCATCTTAATGG	GAGGAAGTACAGTCC	AAAGCAACACATTTA
v.2	TCAGGAAATCTACT	GCCATGTTTCACATA	CAGCTAATTCCTGGA	AGTTTCATCTTAATGG	GAGGAAGTACAGTCC	AAAGCAACACATTTA
v.3	TCAGGAAATCTACT	GCCATGTTTCACATA	CAGCTAATTCCTGGA	AGTTTCATCTTAATGG	GAGGAAGTACAGTCC	AAAGCAACACATTTA
1441	1455 1456	1470 1471	1485 1486	1500 1501	1515 1516	1530
v.1	TATTTGACACATTT	GGCATGTATAGATGT	ACTAATTCAGCTTCAG	AGTTACAGGACAGAA	GTCGACAGACTTGT	GCAAAATTTGTACAGT
v.2	TATTTGACACATTT	GGCATGTATAGATGT	ACTAATTCAGCTTCAG	AGTTACAGGACAGAA	GTCGACAGACTTGT	GCAAAATTTGTACAGT
v.3	TATTTGACACATTT	GGCATGTATAGATGT	ACTAATTCAGCTTCAG	AGTTACAGGACAGAA	GTCGACAGACTTGT	GCAAAATTTGTACAGT
1531	1545 1546	1560 1561	1575 1576	1590 1591	1605 1606	1620
v.1	TCTAGTCCCTAATTT	TATGTATT--TTGGG	AACTCTCTG--	CTTATTTATCTCTGCA	GTCACAGACTTGAGA	GCAATTAATGCAAC
v.2	TCTAGTCCCTAATTT	TATGTATT--TTGGG	AACTCTCTG--	CTTATTTATCTCTGCA	GTCACAGACTTGAGA	GCAATTAATGCAAC
v.3	TCTAGTCCCTAATTT	TATGTATT--TTGGG	AACTCTCTG--	CTTATTTATCTCTGCA	GTCACAGACTTGAGA	GCAATTAATGCAAC
1621	1635 1636	1650 1651	1665 1666	1680 1681	1695 1696	1710
v.1	CTAAATGAGAAATG	GAAATCCCTGACAGCT	GTGTCCGATTCACAGC	ATCAGTCTCTCAAC	AGTTCCCCAGAGCTG	ACAGTCTAGTCTCT
v.2	CTAAATGAGAAATG	GAAATCCCTGACAGCT	GTGTCCGATTCACAGC	ATCAGTCTCTCAAC	AGTTCCCCAGAGCTG	ACAGTCTAGTCTCT
v.3	CTAAATGAGAAATG	GAAATCCCTGACAGCT	GTGTCCGATTCACAGC	ATCAGTCTCTCAAC	AGTTCCCCAGAGCTG	ACAGTCTAGTCTCT
1711	1725 1726	1740 1741	1755 1756	1770 1771	1785 1786	1800
v.1	TTTAAATGTAATG	GAGACTTTGGCATTA	TTTTTCAGATGAAGAT	GTTTCCCAACACTG	TTTACAGATGAGAT	GTGACTC-TACAGAT
v.2	TTTAAATGTAATG	GAGACTTTGGCATTA	TTTTTCAGATGAAGAT	GTTTCCCAACACTG	TTTACAGATGAGAT	GTGACTC-TACAGAT
v.3	TTTAAATGTAATG	GAGACTTTGGCATTA	TTTTTCAGATGAAGAT	GTTTCCCAACACTG	TTTACAGATGAGAT	GTGACTC-TACAGAT
1801	1815 1816	1830 1831	1845 1846	1860 1861	1875 1876	1890

v.1	ACCCTCATAGACACA	ATCCAGATCATACT	TCATTAATCTTGACAG	AGTACGTGTCTTAAA	GGAGCATCATAGAAI	TCATTAATTTGCTTT					
v.2	ACCTCATAG-----	-----	-----	-----	-----	-----					
v.3	ACCTCATAG-----	-----	-----	-----	-----	-----					
1891	1905	1906	1920	1921	1935	1936	1950	1951	1965	1966	1980
v.1	AAAAATACTTTTAA	GGCAATTTTATATA	AGCCAGTCTGGAAA	ACTGAATTTTTTTTA	TTATGTATATATATC	TCGACACCCAGCTTC					
v.2	-----	-----	-----	-----	-----	-----					
v.3	-----	-----	-----	-----	-----	-----					
1981	1995	1996	2010	2011	2025	2026	2040	2041	2055	2056	2070
v.1	TGGATATGCTGCTTT	CTTTTACAGAAAT	ACTACCCACAGATT	TCAGGAAGTACTAGT	AGTTATCCCAAAAGT	GGAAATAGCATGTAT					
v.2	-----	-----	-----	-----	-----	-----					
v.3	-----	-----	-----	-----	-----	-----					
2071	2085	2086	2100	2101	2115	2116	2130	2131	2145	2146	2160
v.1	TCCTAAGTGTTCAG	AAATGTTTATTTCA	CACATAGTCTTAAT	GTATTTGTTATGATT	ATACTTTATAAACA	CTTTTCCAGATGCT					
v.2	-----	-----	-----	-----	-----	-----					
v.3	-----	-----	-----	-----	-----	-----					
2161	2175	2176	2190	2191	2205	2206	2220	2221	2235	2236	2250
v.1	ACAGGTTTGTGATC	TCAAATGTTTACATT	TTCAATTTTGTAAAT	CTTAGAACCAAAATCT	TTATTTATTGTGTC	ACTGTTTATAAATGA					
v.2	-----	-----	-----	-----	-----	-----					
v.3	-----	-----	-----	-----	-----	-----					
2251	2265	2266	2280	2281	2295	2296	2310	2311	2325	2326	2340
v.1	TTTAGGAATACATT	CAATATTATCTGAA	TGGCTGAGTATGTC	TTAAACTCAAAATTC	TATATGATGATTTAA	AACAAAAATAAAGAG					
v.2	-----	-----	-----	-----	-----	-----					
v.3	-----	-----	-----	-----	-----	-----					
2341	2355	2356	2370								
v.1	CGAGGATGGGAAA	AAAAAAAAAAAAAA	AAA	2364							
v.2	-----	-----	-----	1548							
v.3	-----	-----	-----	1557							